



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Patent

In re patent application of: AGUERA et al.

Serial No.: 09/367,496

Examiner: Rawlings

Filed: August 17, 1999

Art Unit: 1642

For: USE OF ULIP PROTEINS IN THE DIAGNOSIS AND THERAPY OF CANCERS AND PARANEOPLASTIC... Docket #: P06473US0/BAS

STATEMENT UNDER 37 CFR §1.821

Commissioner for Patents
Washington, D.C.

S I R:

I hereby certify in accordance with 37 CFR §1.821(f) that the content of the enclosed paper sequence listing and computer readable form of the sequence listing are the same. In accordance with 37 CFR §1.821(g), I hereby certify that the enclosed submission contains no new matter.

Respectfully submitted,

Date: March 25, 2002

By: 
B. Aaron Schulman
Registration No. 31,877

LARSON & TAYLOR PLC
Transpotomac Plaza
1199 North Fairfax Street, Suite 900
Alexandria, Virginia 22314
(703) 739-4900

alignement des cDNA humains Ulip1-4

hUlip-1
hUlip-2
hUlip-3
hUlip-4

ATGTCCTACCAAGGCAAGAAGAACATCCCGGGATCACGAGTGACCGTCT
ATGTCTTATCAGGGGAAGAAAATATTCACGCATCACGAGCGATCGTCT
ATGTCGTACCAGGGCAAGAAGAGCATCCCGCACATCACGAGTGACCGACT
ATGTCCTTCCAGGGCAAGAAAAGCATCCCCGGATCACGAGTGACCGCCT

hUlip-1
hUlip-2
hUlip-3
hUlip-4

CCTTATCAAGGGAGGCAGAATCGTCAATGATGATCAGTCCTTTATGCTG
TCTGATCAAAGGAGGTAAATTTGTTAATGATGACCACTCGTTCTATGCAG
CCTCATCAAAGGTGGACGGATCATCAACGATGACCAATCCCTTTATGCTG
TCTGATCAGAGGTGGAGGATCGTGAATGACGACCACTCCTTTTACGCTG

hUlip-1
hUlip-2
hUlip-3
hUlip-4

ATATTTACATGGAAGATGGCTTAATAAAACAAATTGGAGACAATCTGATT
ACATATACATGGAAGATGGGTTGATCAAGCAAATAGGAGAAAATCTGATT
ACGTCTACCTGGAGGATGGACTTATCAAACAAATAGGAGAGAACTTAATC
ATGTGCACGTGGAAGATGGCTTGATAAAACAAATCGGAGAAAACCTCATC

hUlip-1
hUlip-2
hUlip-3
hUlip-4

GTTCTGGAGGAGTGAAGACCATTGAAGCCAATGGGAAGATGGTGATCCC
GTGCCAGGAGGAGTGAAGACCATTGAAGCCAATGGGAAGATGGTGATCCC
GTTCTGGTGGAGTGAAGACCATTGAAGCCAATGGGAAGATGGTGATCCC
GTCCCTGGGGGCATCAAGACCATTGACGCCACGGCCTGATGGTCTCTCC

hUlip-1
hUlip-2
hUlip-3
hUlip-4

TGGAGGCATCGATGTCCATACTCACTTCCAGATGCCATATAAGGGAATGA
CGGAGGAATTGACGTCCACACTCGTTTCCAGATGCCATAGGGAATGA
CGGAGGTATTGATGTCAACAGTACCTGCAGAGCCCTCCAGGGGATGA
TGGTGGCGTTGACGTCCACACAAGGCTGCAGATGCCCTGTCTGGGCATGA

hUlip-1
hUlip-2
hUlip-3
hUlip-4

CCACAGTAGATGACTTCTTCCAAGGGACAAAGGCGGCCCTTAGCAGGTGGC
CGTCTGCTGATGATTTCTTCCAAGGAACCAAGGCGGCCCTGGCTGGGGGA
CTGCCGCTGATGACTTCTTCCAAGGGAACCAAGGCGGCCCTGGCTGGGGGA
CACCAGCTGACGACTTCTGTGAGGGCACCAGGCGCTAGCAGGAGGA

hUlip-1
hUlip-2
hUlip-3
hUlip-4

ACCACCATGATCATTGACCATGTGGTGCCTGAGCCTGAGTCCAGCCTGAC
ACCACTATGATCATTGACCACGTTGTTCTGAGCCTGGGACAAGCCTGCT
ACCACGATGATCATTGACCATGTTGTTCTGAACCTGGGTCCAGCCTACT
ACCACCATGATCTTGGACCACGTTCTTCCCGACAGGGGTGTGAGCCTGCT

hUlip-1
hUlip-2
hUlip-3
hUlip-4

TGAGGCCATAGAGAAATGGAGAGAGTGGGCTGATGGGAAGAGTTGCTGTG
CGCTGCCCTTGACCAAGTGGAGGGAATGGGCCGACAGCAAGTCTGCTGTG
GACCTCTTTCGAGAAGTGGCACGAAGCAGCTGACACCAATCTGCTGTG
GGCGGCCCTACGAGCGGTGGCGGGAGCGGGCGGACAGCGGCCCTGCTGCG

hUlip-1
hUlip-2
hUlip-3
hUlip-4

ACTATGCCCTGCATGTGGACATCACCCACTGGAATGACAGCGTCAAGCAG
ACTACTCTCTGCATGTGGACATCAGCGAGTGGCATAAGGGCATCCAGGAG
ATTACTCCCTCCACGTGGACATCACAAGCTGGTACGATGGCGTTCGGGAG
ACTACTCCCTGCACGTGGACATCACCCATGGCATGAGAGCATCAAGGAG

hUlip-1
hUlip-2
hUlip-3
hUlip-4

GAAGTGCAGAACCTCATCAAGGACAAAGGGGTTAACTCCTTCATGGTTTA
GAGATGGAAGCGCTTGTGAAGGATCACGGGGTAAATTCCTTCCTCGTGTA
GAGCTGGAGGTGCTGGTGCAGGACAAAGCGTCAATTCCTTCCAAGTCTA
GAGCTGGAGGCCCTGGTCAAGGAGAGGGTGTGAACCTCCTTCCTGCTCT

hUlip-1
hUlip-2
hUlip-3
hUlip-4

TATGGCTTATAAGGATTTGTATCAAGTATCTAACACAGAGCTCTATGAGA
CATGGCTTTCAAAGATCGCTTCCAGCTAACGGATTGCCAGATTATGAAG
CATGGCCTATAAGGATGTCTACCAATGTCCGACAGCCAGCTCTATGAAG
CATGGCATAACAAGGACCGGTGCCAGTGCAGCGACAGCCAGATGTACGAGA

hUlip-1
hUlip-2
hUlip-3
hUlip-4

TCTTCACCTGCCTGGGAGAGCTGGGGGCCATTGCTCAAGTTCATGCTGAG
TACTGAGTGTGATCCGGGATATTGGCGCCATAGCCCAAGTCCACGCAGAA
CCTTTACCTTCTTAAGGGCCTGGGAGCTGTGATCTTGGTCCATGCAGAA
TCTTCAGCATCATCCGGGACCTGGGGGCCTTGGCCAGGTGCACGCTGAG

hUlip-1
hUlip-2
hUlip-3
hUlip-4

AATGGGGATATCATTGCCAGGAGCAAACCCGCATGTTGGAAATGGGGAT
AATGGCGACATCATTGCAGAGGAGCAGCAGAGGATCCTGGATCTGGGCAT
AATGGAGATTTGATAGCTCAGGAACAAAGCGGATCCTGGAGATGGGCAT
AACGGGGACATCGTGGAGGAGGAGCAGAAGCGGTTGCTGGAGCTCGGCAT

hUlip-1
hUlip-2
hUlip-3
hUlip-4

AACTGGCCCAGAAGGCCATGTACTGAGCAGGCCAGAAGAGCTGGAAGCTG
CACGGGCCCCGAGGGACATGTGCTGAGCCGACCTGAGGAGGTGAGGCCG
CACGGGTCCCGAGGGCCATGCCCTGAGCAGACCTGAAGAGCTGGAGGCCG
CACTGGCCCCGAGGGCCACGTGCTCAGCCACCCCGAGGAGGTGAGGCTG

hUlip-1
hUlip-2
hUlip-3
hUlip-4

AGGCTGTGTTCCGTGCCATCACCATTGCCAGCCAAACCAATTGCCCTCTC
AAGCCGTGAATCGTGCCATCACCATCGCCAACCAAGACCAACTGCCCGCTG
AGGCGGTGTTCCGGGCCATCACCATTGCGGGCCGGATCAACTGCCCTGTG
AGGCGGTGTACCGAGCTGTACCATCGCCAAGCAGGCAAACTGCCCGCTG

hUlip-1
hUlip-2
hUlip-3
hUlip-4

TACGTACAAAGGTTCATGAGCAAGAGTGCAGCTGACCTCATCTCACAAGC
TATATCAACCAAGGTGATGAGCAAAAGCTCTGCTGAGGTCTCGCCAGGC
TACATCAACCAAGGTTCATGAGCAAGAGTGCAGCCGACATCATCGCTCTGGC
TACGTACCAAGGTGATGAGCAAGGGGCGGCCGACCCATCGCTCAGGC

hUlip-1
hUlip-2
hUlip-3
hUlip-4

CAGGAAAAAGGAAATGTAGTCTTTGGTGAGCCCATCACTGCCAGCCTCG
ACGGAAGAAGGGAAGTGTGGTGATGGCGAGCCCATCACTGCCAGCTTGG
CAGGAAGAAAGGGCCCTAGTTTTTGGAGAGCCCATTGCCCGCAGCCTGG
CAAGCGCAGAGGGGTGGTGTGTTTGGGAGCCCATACCGCCAGCCTGG

hUlip-1
hUlip-2
hUlip-3
hUlip-4

GCATAGATGGAACCCATTATTGGAGCAAGAACTGGGCCAAGGCGGCTGCA
GAACGGACGGCTCCCATTACTGGAGCAAGAACTGGGCCAAGGCTGCTGCC
GGACCGATGGCACCCATTACTGGAGCAAGAACTGGGCCAAGGCTGCGGCC
GCACCGACGGTTCACACTACTGGAGCAAGAACTGGGCCAAGGCCGAGCC

hUlip-1
hUlip-2
hUlip-3
hUlip-4

TTTGTGACATCCCCACCCTGAGCCCTGACCCAACCTACTCCGGACTACAT
TTTGTACCTCCCCACCCTTGGAGCCCTGATCCAACCACTCCAGACTTTCT
TTCGTGACTTCCCCTCCCCTGAGCCCGGACCCATACCAGGCCGACTACTT
TTCGTACATCACCCTGTCAACCCAGACCCACCCAGGCCAGACCCT

hUlip-1
hUlip-2
hUlip-3
hUlip-4

CAACTCCTTGCTGGCCAGCGGGGATCTGCAGCTATCTGGGAGTGGCCACT
CAACTCCTTGCTGTCTGTGGAGACCTCCAGGTCACGGGCAGTGCCCAT
GACCTCCCTACTGGCCTGTGGGGACTTGCAAGTACAGGCAGCGGCCACT
CACCTGCTTGCTGTCCAGCGGGGACCTCCAGGTGACAGGCAGCGGCCACT

hulip-1
hulip-2
hulip-3
hulip-4

GCACCTTCAGCACTGCCAGAAAGCAATTGGGAAGGACAACCTTCACAGCC
GCACGTTTTAACTGCCAGAAAGGCTGTAGGAAAGGACAACCTTCACCCTG
GTCCCTACAGCACTGCCAGAAAGGCGGTGGGCAAGGACAACCTTACCCTG
GCACCTTCACCCTGCCAGAAAGGCTGTGGGCAAGGACAACCTTCGCGCTG
* * * * *

hulip-1
hulip-2
hulip-3
hulip-4

ATTCCCTGAGGGCACCAATGGTGTGGAGGAGCGGATGTCTGTCTCTGGGA
ATTCCGGAGGGCACCAATGGCACTGAGGAGCGGATGTCCGTCTCTGGGA
ATCCCCGAGGGTGTCAACGGGATAGAGGAGCGGATGACCGTCTCTGGGA
ATCCCCGAGGGCACCAACGGCATTGAGGAGCGCATGTCTGTCTGGGA
* * * * *

hulip-1
hulip-2
hulip-3
hulip-4

CAAGGCTGTGGCCACAGGGAAAATGGACGAAAACCAAGTTCGTGGCTGTGA
CAAGGCTGTGGTCACTGGGAAGATGGATGAGAACCAGTTGTGGCTGTGA
CAAGGCGGTGGCTACTGGCAAATGGATGAGAACCAGTTGTCTGTCTGA
GAAATGTGTGGCTCTGGGAAGATGGACGAGAATGAGTTCGTCTGGCTGA
* * * * *

hulip-1
hulip-2
hulip-3
hulip-4

CAAGCACAAACGCTGCCAAGATCTTCAACCTGTATCCCCGCAAGGGAAGA
CCAGCACCAATGCAGCCAAAGTCTTCAACCTTTACCCCCGGAAGGCGCG
CCAGCACCAATGCAGCCAAAGATCTTTAACCCTGTACCCAAGGAAAGGCGG
CCAGTACAAATGCTGCCAAAATCTTCAATTTTACCCAAGGAAAGGCGGA
* * * * *

hulip-1
hulip-2
hulip-3
hulip-4

ATATCTGTGGGTTCTGACAGCGACCTCGTCTCTGGGATCCAGATGCTGT
ATTGCTGTGGGATCCGATGCCGACCTGGTCTCTGGGACCCCGACAGCGT
ATTGCCGTGGGCTCGGATGCCGACCTGGTCTCTGGGACCCCGACAAGTT
GTGGCTGTGGGCTCTGACGCTGACCTGGTCTATGGAACCCCAAGGCCAC
* * * * *

hulip-1
hulip-2
hulip-3
hulip-4

GAAGATCGTCTCTGCCAAGAACCACAGTCTGCGGCAGAGTACAACATCT
TAAAACCATCTCTGCCAAGACACACAACAGCTCTCTCGAGTACAACATCT
GAAGACCATAACAGCCAAAGTCAACAAGTCGCGGCTGGAGTACAACATCT
CAAGATCATCTCTGCCAAGACCCACAATCTGAACGTGGAGTACAACATCT
* * * * *

hulip-1
hulip-2
hulip-3
hulip-4

TTGAAGGGATGGAGCTGCGCGGGGCTCCTCTGGTTGTCTCTGCCAGGGC
TTGAAGGCATGGAGTGCCGCGGCTCCCCACTGGTGGTCTCTAGCCAGGGG
TCGAGGGTATGGAGTGCCACGGCTCCCCACTAGTGGTCTCTAGCCAGGGC
TCGAGGGAGTGGAGTGCCGCGGAGCGCCTGCCGTGGTCTAAGTCAAGGGC
* * * * *

hulip-1
hulip-2
hulip-3
hulip-4

AAGATCATGCTGGAAGATGGCAACCTGCACGTGACCCAGGGGCTGGCCG
AAGATTGCTCCTGGAGGACGGCACCTGCATGTACCCGAAGGCTCTGGACG
AAGATCGTCTTTGAAGACGGAACATCAACGTCAACAAGGGCATGGGCGG
CGAGTGGCGCTGGAGGACGGGAAGATGTTGTACCCCGGGGGCGGGCCG
* * * * *

hulip-1
hulip-2
hulip-3
hulip-4

CTTCATACCCTGCAGCCCGTTCTCCGACTATGTCTACAAGCGCATTAAAG
CTACATTCCCCGGAAGCCCTTCCCTGATTTTGTCTACAAGCGTATCAAGG
CTTCATTCCGCGGAAGGCGTTCCCGGAGCACCTGTACCAGCGCGTCAAAA
CTTCGTCCTCGGAAAACATTCCCGGACTTTGTCTACAAGAGGATCAAG
* * * * *

hulip-1
hulip-2
hulip-3
hulip-4

CACGGAGGAAGATGGCAGACCTGCATGCCGTCCCAAGGGGCATGTACGAT
CAAGGAGCAGGCTGGCTGAGCTGAGAGGGGTTCCCTCGTGGCCTGTATGAC
TCAGGAATAAGGTTTGTGATTGCAAGGGGTTTCAGGGGCATGTATGAC
CTCGCAACAGGCTGGCGGAGATCCACGGTGTGCCCGTGGGCTGTATGAC
* * * * *

hUlip-1 GGGCCTGTGTTTGACCTGACCACCACCCCAAAGGTGGGACCCCGCAGG
hUlip-2 GGACCTGTGTGTGAAGTGTCTGTGACGCCCCAAGACAGTCACTCCAGCCTC
hUlip-3 GGTCTGTGTACGAGGTACCAGCTACACCCAAATATGCAACTCCCGCTCC
hUlip-4 GGGCCCGTCCACGAGGTGATGGTGCCTGCCAAGCCAGGGAGTGGCGCTCC
* * * * *

hUlip-1 CTCTGCTCGGGGCTCTCCTACT---CGGCCGAACCCACCTGTGAGGAATC
hUlip-2 CTCGGCCAAGACGTCTCCTGCCAAGCAGCAGGCCCCACCTGTCCGGAACC
hUlip-3 TTCAGCCAAATCTTCGCCTTCTAAACACCAGCCCCACCCATCAGAAACC
hUlip-4 GGCCCGCGCGTCTCTGCCAGGCAAGATCTCCGTGCCTCTCTGTGCGCAACC
* * * * *

hUlip-1 TTCATCAGTCGGGATTTAGCCTGTGAGGCACCCAAAGTGGATGAGGGGGTT
hUlip-2 TGCACCACTCTGATTTCAGTTTGTCTGGTGCTCAGATTGATGACAACATT
hUlip-3 TCCACCAGTCCAACTTCAGCTTATCAGGTGCCAGATAGATGACAAACAT
hUlip-4 TACATCAGTCGGGGTTTACGCTATCTGGGTCTCAGGCTGATGACCACATC
* * * * *

hUlip-1 C---GCTCAGCCAGCAAGCGCATCGTGGCCCCCCCAGGCGGCCGTTCTAA
hUlip-2 CCCCCGCCGACCCACCCAGCGTATCGTGGCGCCCCCGGTGGCCGTGCCAA
hUlip-3 CCCAGGCGCACCCGCCACCGCATCGTGGCGCCCCCTGGTGGCCGCTCCAA
hUlip-4 GCCCCAGCGCACAGCACAGAAGATCATGGCACCACCTGGCGGCCGCTCCAA
* * * * *

hUlip-1 TATCACATCTCTGAGTTAA
hUlip-2 CATCACCAGCCTGGGCTAG
hUlip-3 CATCACCAGCCTCGGTTGA
hUlip-4 CATCACCTCTCTCTCCTAG

Sequences (U1:U2) Aligned. Score: 68.7682
Sequences (U1:U3) Aligned. Score: 67.0169
Sequences (U1:U4) Aligned. Score: 64.6235
Sequences (U2:U3) Aligned. Score: 70.1571
Sequences (U2:U4) Aligned. Score: 69.0518
Sequences (U3:4) Aligned. Score: 65.2705